SEQUENCE LISTING

<110> Genodyssee

<120> New polynucleotides and polypeptides of the IFNalpha-5 gene

<130> IFNa-5

<140>

<141>

<160>2

<170> PatentIn Ver. 2.1

<210>1

<211> 1475

<212> ADN

<213> Homo sapiens

<400> 1

cttaatccgg gactgaataa attctatttt acattctatt acgctgcttt taaagcatta 60 aagaagtaca atattetete tegataatgg gtaetgtaat gtatatacat eageeaacae 120 atagtatatc tgtgttatta aaatttaatg ggatttttag ttagaaaaaa aatttctaaa 180 ctcctgtaca tctatgtaga aagagcataa aagaaagcaa aaagagaagt agaaagtaac 300 acaaggcatt cagaaaatgg aaactcgtat gtgacctttt taagatctgt gcacaaaaca 360 aggtetteag agaagageee aaggtteagg gteacteaat eteaacagee eagaageate 420 tgcaacctcc ccaatggcct tgccctttgt tttactgatg gccctggtgg tgctcaactg 480 caagtcaatc tgttctctgg gctgtgatct gcctcagacc cacagcctga gtaacaggag 540 gactttgatg ataatggcac aaatgggaag aatctctcct ttctcctgcc tgaaggacag 600 acatgacttt ggattteete aggaggagtt tgatggeaac eagtteeaga aggeteaage 660 catetetgte etceatgaga tgatecagea gacetteaat etetteagea caaaggaete 720 atetgetaet tgggatgaga eaettetaga eaaattetae aetgaaettt aeeageaget 780 gaatgacetg gaageetgta tgatgeagga ggttggagtg gaagacacte etetgatgaa 840 tgtggactet ateetgactg tgagaaaata ettteaaaga ateaceetet atetgacaga 900 gaagaaatac agccettgtg catgggaggt tgtcagagca gaaatcatga gatcettete 960 tttatcagca aacttgcaag aaagattaag gaggaaggaa tgaaaactgg ttcaacatcg 1020 aaatgattet cattgactag tacaccattt cacacttett gagttetgee gtttcaaata 1080 ttaatttctg ctatatccat gacttgagtt gaatcaaaat tttcaaacgt ttcacacgtg 1140 ttaagcaaca ettetttage teeacaggga caaaatettt acagatgate atgecaatet 1200 atctattcta tctatttatc tatctgtctg tcttctatct aatctattta aatatttatt 1260 tactttgtgg ctaatataat aaaatatgtt ctttatgttt tgtcaactga ttattttgct 1380 ttgttcatta gatttttact attaattgtt tgtttattct ttaaaatgaa actccaagcc 1440 1475 tgattgtata acttgattaa aaacagatgg tacag

<211> 189 <212> PRT <213> Homo sapiens <400> 2 Met Ala Leu Pro Phe Val Leu Leu Met Ala Leu Val Val Leu Asn Cys 15 10 Lys Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu 25 Ser Asn Arg Arg Thr Leu Met Ile Met Ala Gln Met Gly Arg Ile Ser 45 40 Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu 55 Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Gln Ala Ile Ser Val Leu 70 75 65 His Glu Met Ile Gln Gln Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser 90 Ser Ala Thr Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu 105 Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Met Met Gln Glu Val Gly 115 Val Glu Asp Thr Pro Leu Met Asn Val Asp Ser Ile Leu Thr Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser 155 Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser 165 170 175 Leu Ser Ala Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu 180 185 SEQ ID NO. 3: ggtcactcaatctcaacagc SEQ ID NO. 4: ggcagaactcaagaagtgtg

SEQ ID NO. 5: tctgggctgtgatctgcctc

SEQ ID NO. 6: tgttactcaggctgtgggtc

SEQ ID NO. 7: aggaggagtttgatggcaac

SEQ ID NO. 8: ggcttgagccttctggaact

SEQ ID NO. 9: gctgaatgacctggaagcct

SEQ ID NO. 10: ctccaacctcctgcatcata

SEQ ID NO. 11: tgtgatctgcctcagacccac

SEQ ID NO. 12: tcattccttcctccttaatctttcttg